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RAW SEQUENCE LISTING                      DATE: 02/10/2002  
PATENT APPLICATION: US/10/016,403              TIME: 13:47:22

Input Set : N:\Crf3\RULE60\10016403.txt  
Output Set: N:\CRF3\02102002\J016403.raw

## SEQUENCE LISTING

## 4 (1) GENERAL INFORMATION:

6        (i) APPLICANT: Holladay, Leslie A.  
8        (ii) TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE DRUGS TO  
9    INCREASE ELECTROTRANSPORT FLUX  
11       (iii) NUMBER OF SEQUENCES: 10  
13       (iv) CORRESPONDENCE ADDRESS:  
14                (A) ADDRESSEE: Stroud, Willink, Thompson & Howard  
15                (B) STREET: 25 West Main Street  
16                (C) CITY: Madison  
17                (D) STATE: WI  
18                (E) COUNTRY: USA  
19                (F) ZIP: 53701-2236

## 21       (v) COMPUTER READABLE FORM:

22                (A) MEDIUM TYPE: Floppy disk  
23                (B) COMPUTER: IBM PC compatible  
24                (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
25                (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

## 27       (vi) CURRENT APPLICATION DATA:

C--> 28                (A) APPLICATION NUMBER: US/10/016,403  
C--> 29                (B) FILING DATE: 10-Dec-2001  
35                (C) CLASSIFICATION:

## C--&gt; 32       (vii) PRIOR APPLICATION DATA:

33                (A) APPLICATION NUMBER: 08/466,610  
34                (B) FILING DATE: 1995-JUN-06

## 36       (viii) ATTORNEY/AGENT INFORMATION:

37                (A) NAME: Frenchick, Grady J.  
38                (B) REGISTRATION NUMBER: 29,018  
39                (C) REFERENCE/DOCKET NUMBER: 8734.28

## 41       (ix) TELECOMMUNICATION INFORMATION:

42                (A) TELEPHONE: 608-257-2281  
43                (B) TELEFAX: 608-257-7643

## 46 (2) INFORMATION FOR SEQ ID NO: 1:

## 48       (i) SEQUENCE CHARACTERISTICS:

49                (A) LENGTH: 174 amino acids  
50                (B) TYPE: amino acid  
51                (D) TOPOLOGY: linear

## 54       (ix) FEATURE:

55                (A) NAME/KEY: Peptide  
56                (B) LOCATION: 1..174  
57                (D) OTHER INFORMATION: /note= "granulocyte-colony  
58 stimulating factor"

## 61       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ENTERED

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```

63   Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys
64   1           5           10           15
66   Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln
67           20           25           30
69   Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val
70           35           40           45
72   Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
73           50           55           60
75   Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser
76   65           70           75           80
78   Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
79           85           90           95
81   Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
82           100          105          110
84   Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro
85           115          120          125
87   Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
88           130          135          140
90   Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
91   145          150          155          160
93   Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
94           165          170

```

96 (2) INFORMATION FOR SEQ ID NO: 2:

98 (i) SEQUENCE CHARACTERISTICS:

99 (A) LENGTH: 174 amino acids

100 (B) TYPE: amino acid

101 (D) TOPOLOGY: linear

104 (ix) FEATURE:

105 (A) NAME/KEY: Peptide

106 (B) LOCATION: 1..174

107 (D) OTHER INFORMATION: /note= "modified granulocyte-colony  
108 stimulating factor"

111 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

113   Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro His Ser Phe Leu Leu Lys
114   1           5           10           15
116   Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln
117           20           25           30
119   Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val
120           35           40           45
122   Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
123           50           55           60
125   Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser
126   65           70           75           80
128   Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
129           85           90           95
131   Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
132           100          105          110
134   Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro
135           115          120          125

```

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```

137      Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
138          130                      135                      140
140      Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
141          145                      150                      155                      160
143      Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
144          165                      170

```

146 (2) INFORMATION FOR SEQ ID NO: 3:

148 (i) SEQUENCE CHARACTERISTICS:

149 (A) LENGTH: 174 amino acids

150 (B) TYPE: amino acid

151 (D) TOPOLOGY: linear

154 (ix) FEATURE:

155 (A) NAME/KEY: Peptide

156 (B) LOCATION: 1..174

157 (D) OTHER INFORMATION: /note= "modified granulocyte-colony  
158 stimulating factor"

161 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

163      Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro His Ser Phe Leu Leu Lys
164          1          5          10          15
166      Cys Leu Glu His Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln
167          20          25          30
169      Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val
170          35          40          45
172      Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
173          50          55          60
175      Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser
176          65          70          75          80
178      Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
179          85          90          95
181      Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
182          100         105         110
184      Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro
185          115         120         125
187      Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
188          130         135         140
190      Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
191          145         150         155         160
193      Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
194          165         170

```

196 (2) INFORMATION FOR SEQ ID NO: 4:

198 (i) SEQUENCE CHARACTERISTICS:

199 (A) LENGTH: 174 amino acids

200 (B) TYPE: amino acid

201 (D) TOPOLOGY: linear

204 (ix) FEATURE:

205 (A) NAME/KEY: Peptide

206 (B) LOCATION: 1..174

207 (D) OTHER INFORMATION: /note= "granulocyte-colony  
208 stimulating factor"

## RAW SEQUENCE LISTING

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Input Set : N:\Crf3\RULE60\10016403.txt

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211 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
213 Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys
214 1 5 10 15
216 Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln
217 20 25 30
219 Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val
220 35 40 45
222 Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
223 50 55 60
225 Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser
226 65 70 75 80
228 Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
229 85 90 95
231 Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu His Leu Asp Val Ala Asp
232 100 105 110
234 Phe Ala Thr Thr Ile Trp His His Met Glu Glu Leu Gly Met Ala Pro
235 115 120 125
237 Ala Leu His Pro Thr His Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
238 130 135 140
240 His Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu His Ser Phe
241 145 150 155 160
243 Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala His Pro
244 165 170
246 (2) INFORMATION FOR SEQ ID NO: 5:
248 (i) SEQUENCE CHARACTERISTICS:
249 (A) LENGTH: 34 amino acids
250 (B) TYPE: amino acid
251 (D) TOPOLOGY: linear
254 (ix) FEATURE:
255 (A) NAME/KEY: Peptide
256 (B) LOCATION: 1..34
257 (D) OTHER INFORMATION: /note= "parathyroid hormone"
260 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
262 Ser Val Ser Glu Ile Gln Leu Met His Asn Leu Gly Lys His Leu Asn
263 1 5 10 15
265 Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val His
266 20 25 30
268 Asn Phe
271 (2) INFORMATION FOR SEQ ID NO: 6:
273 (i) SEQUENCE CHARACTERISTICS:
274 (A) LENGTH: 34 amino acids
275 (B) TYPE: amino acid
276 (D) TOPOLOGY: linear
279 (ix) FEATURE:
280 (A) NAME/KEY: Peptide
281 (B) LOCATION: 1..34
282 (D) OTHER INFORMATION: /note= "modified parathyroid
283 hormone"
286 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

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Output Set: N:\CRF3\02102002\J016403.raw

```

288   Ser Val Ser Glu Ile His Leu Met His Asn Leu Gly Lys His Leu Asn
289   1           5           10           15
291   Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val His
292           20           25           30
294   Asn Phe
297 (2) INFORMATION FOR SEQ ID NO: 7:
299   (i) SEQUENCE CHARACTERISTICS:
300       (A) LENGTH: 34 amino acids
301       (B) TYPE: amino acid
302       (D) TOPOLOGY: linear
305   (ix) FEATURE:
306       (A) NAME/KEY: Peptide
307       (B) LOCATION: 1..34
308       (D) OTHER INFORMATION: /note= "modified parathyroid
309 hormone"
312   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
314   Ser Val Ser Glu Ile Gln Leu Met His Asn Leu Gly Lys His Leu Asn
315   1           5           10           15
317   Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu His Asp Val His
318           20           25           30
320   Asn Phe
323 (2) INFORMATION FOR SEQ ID NO: 8:
325   (i) SEQUENCE CHARACTERISTICS:
326       (A) LENGTH: 44 amino acids
327       (B) TYPE: amino acid
328       (D) TOPOLOGY: linear
331   (ix) FEATURE:
332       (A) NAME/KEY: Peptide
333       (B) LOCATION: 1..44
334       (D) OTHER INFORMATION: /note= "human growth hormone
335 releasing hormone"
337   (ix) FEATURE:
338       (A) NAME/KEY: Binding-site
339       (B) LOCATION: 44
340       (D) OTHER INFORMATION: /note= "carboxy terminal amide"
343   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
345   Tyr Ala Asp Ala Ile Phe Thr Asn Ser Tyr Arg Lys Val Leu Gly Gln
346   1           5           10           15
348   Leu Ser Ala Arg Lys Leu Leu Gln Asp Ile Met Ser Arg Gln Gln Gly
349           20           25           30
351   Glu Ser Asn Gln Glu Arg Gly Ala Arg Ala Arg Leu
352           35           40
354 (2) INFORMATION FOR SEQ ID NO: 9:
356   (i) SEQUENCE CHARACTERISTICS:
357       (A) LENGTH: 44 amino acids
358       (B) TYPE: amino acid
359       (D) TOPOLOGY: linear
362   (ix) FEATURE:
363       (A) NAME/KEY: Peptide

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## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/016,403

DATE: 02/10/2002

TIME: 13:47:24

Input Set : N:\Crf3\RULE60\10016403.txt

Output Set: N:\CRF3\02102002\J016403.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:32 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]